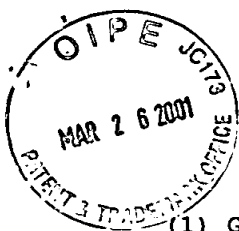


SEQUENCE LISTING



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(1) GENERAL INFORMATION:

- (i) APPLICANT: Botella, Jose Ramon
- (ii) TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
 - (B) STREET: 100 Thanet Circle, Suite 306
 - (C) CITY: Princeton
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 08540-3662
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/043,627
 - (B) FILING DATE: 20-MAR-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/AU96/00591
 - (B) FILING DATE: 20-SEP-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PN5559
 - (B) FILING DATE: 20-SEP-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PN9603
 - (B) FILING DATE: 02-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Bernstein, Scott N.
 - (B) REGISTRATION NUMBER: 38,827
 - (C) REFERENCE/DOCKET NUMBER: 3573-11US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 609-924-8555
 - (B) TELEFAX: 609-924-3036

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG	ATG	GGG	TTT	GCG	GAG	AAC	CAG	CTT	TCG	CTG	GAG	TTA	ATA	CGT	GAG	48
Gln	Met	Gly	Phe	Ala	Glu	Asn	Gln	Leu	Ser	Leu	Glu	Leu	Ile	Arg	Glu	
1				5					10					15		
TGG	ATC	AAG	AAT	CAC	CCG	GAG	GCC	TCC	ATT	TGC	TCG	GCG	GAG	GGC	CTG	96
Trp	Ile	Lys	Asn	His	Pro	Glu	Ala	Ser	Ile	Cys	Ser	Ala	Glu	Gly	Leu	
			20					25					30			
CCG	CAG	TTC	ATG	GAG	ATC	GCC	AAT	TTC	CAA	GAC	TAC	CAT	GGC	TTG	CCG	144
Pro	Gln	Phe	Met	Glu	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Pro	
		35					40					45				
GCT	TTT	CTG	CAG	GGA	ATC	GCG	AAA	TTG	ATG	GAG	AAA	GTG	AGA	GGA	GGA	192
Ala	Phe	Leu	Gln	Gly	Ile	Ala	Lys	Leu	Met	Glu	Lys	Val	Arg	Gly	Gly	
	50					55					60					
AGG	GTC	AAA	TTC	GAT	CCG	AAC	CGC	GTG	GTG	ATG	AGC	GGC	GGA	GGC	ACT	240
Arg	Val	Lys	Phe	Asp	Pro	Asn	Arg	Val	Val	Met	Ser	Gly	Gly	Gly	Thr	
65					70					75					80	
GGA	GCG	CAA	GAA	ACG	CTC	GCG	TTT	TGT	CTC	GCT	GAC	CCT	GGC	GAC	GCC	288
Gly	Ala	Gln	Glu	Thr	Leu	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	
				85					90					95		
TTC	CTC	GTC	CCA	ACT	CCG	TAC	TAT	CCA	GCA	TTT	AAT	CGC	GAT	CTC	CGG	336
Phe	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Ala	Phe	Asn	Arg	Asp	Leu	Arg	
			100					105					110			
TGG	AGA	ACG	GGC	GTC	GAG	CTC	CTC	CCG	GTT	CAC	TGC	AAG	AGC	TCT	AAT	384
Trp	Arg	Thr	Gly	Val	Glu	Leu	Leu	Pro	Val	His	Cys	Lys	Ser	Ser	Asn	
		115					120					125				
CAC	TTC	AGA	GTC	ACC	AAA	ACG	GCG	CTA	GAA	TCG	GCA	TAC	GAG	AAG	GCG	432
His	Phe	Arg	Val	Thr	Lys	Thr	Ala	Leu	Glu	Ser	Ala	Tyr	Glu	Lys	Ala	
	130					135					140					
CGA	AAG	GAT	AAC	ATC	AGA	GTA	AAA	GGA	GTA	CTG	ATA	ACC	AAC	CCA	TCC	480
Arg	Lys	Asp	Asn	Ile	Arg	Val	Lys	Gly	Val	Leu	Ile	Thr	Asn	Pro	Ser	
145					150					155				160		
AAC	CCG	CTC	GGC	ACG	ACC	ATG	GAT	AAA	CAC	ACG	CTA	CAG	ACC	CTC	GTG	528
Asn	Pro	Leu	Gly	Thr	Thr	Met	Asp	Lys	His	Thr	Leu	Gln	Thr	Leu	Val	
				165					170					175		
AAA	TTC	GTA	AAC	GAA	AGG	AGA	ATC	CAC	CTA	GTC	TGC	GAC	GAG	TTA	TAC	576
Lys	Phe	Val	Asn	Glu	Arg	Arg	Ile	His	Leu	Val	Cys	Asp	Glu	Leu	Tyr	
			180					185					190			
GGC	GCA	ACC	ATC	TTT	AGG	GAG	CCC	AGG	TTC	GTC	AGC	ATC	TCC	GAG	GTA	624
Gly	Ala	Thr	Ile	Phe	Arg	Glu	Pro	Arg	Phe	Val	Ser	Ile	Ser	Glu	Val	
		195					200					205				

ATA GAA GAG GAC CCG AAC TGC GAC AAG AAT CTG ATC CAC ATT GCG TAC Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr 210 215 220	672
AGT CTC TCA AAG GAC TTC GGT CTC CCC GGA TTC CGA GTC GGG ATC GTG Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val 225 230 235 240	720
TAT TCC TAC AAC GAC ACG GTG GTT AGT TGC GCA CGC AGA ATG TCG AGC Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser 245 250 255	768
TTC GGC CTC GTC TCG TCG CAG ACA CAG TAC CTA CTG GCC GCC ATG CTA Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu 260 265 270	816
TCC GGC GAA GAA TTT TTG CCA ACA TTA CTG ACT GAA AGC GCG AAG AGT Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser 275 280 285	864
CTG TCG GAG AGC CAC AGG ATC TTC TCT TCC GGC CTT GAG GAA GTC GAC Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp 290 295 300	912
ATC CGC TGC TTG GAC GGC AAT GCC GGG GTC TTC TGC TGG ATG GAC CTA Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu 305 310 315 320	960
CGG CAC CTC CTC AAA GAA GCC ACC GAA GAC GGC GAG CTC GAG CTG TGG Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp 325 330 335	1008
CGC GTG ATA GTG AAC AAT GTC AAG CTC AAT GTG TCC CCC GGT TCG TCG Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser 340 345 350	1056
TTT TAT TGC GCC GAG CCA GGT TGG Phe Tyr Cys Ala Glu Pro Gly Trp 355 360	1080

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu 1 5 10 15
Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu 20 25 30
Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro 35 40 45

Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
 50 55 60
 Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
 65 70 75 80
 Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
 100 105 110
 Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
 115 120 125
 His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
 130 135 140
 Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
 165 170 175
 Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr
 180 185 190
 Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
 195 200 205
 Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
 210 215 220
 Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
 225 230 235 240
 Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
 245 250 255
 Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
 260 265 270
 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
 275 280 285
 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
 290 295 300
 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
 305 310 315 320
 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
 325 330 335
 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350
 Phe Tyr Cys Ala Glu Pro Gly Trp
 355 360

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAG ATG GGC CTT GCT GAG AAT CAG CTT TGC TTT AAT TTA ATT CAC GAG	48
Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu	
1 5 10 15	
TGG CCG CTG AAA AAC CCA GAA GCC TCC ATT TGT ACA ACA CAA GGA GCA	96
Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala	
20 25 30	
GCT GAA TTC AGA GAT ATA GCT ATC TTT CAA GAT TAT CAT GGC TTG GCT	144
Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala	
35 40 45	
GAA TTC AGA GAG GCT GTT GCA AAG TTT ATG GGG AAA GTG AGA AGA AAC	192
Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn	
50 55 60	
AGA GCT TCA TTT GAC CCT GAT CGG ATT GTT ATG AGT GGA GGA GCA ACT	240
Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr	
65 70 75 80	
GGA GCT CAT GAA ATG ATT GGT TTC TGT TTG GCT GAT CCT GGC GAT GCA	288
Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala	
85 90 95	
TTC TTG GTT CCA ACT CCT TAT TAT CCA GGG TTT GAT AGA GAT TTG AGA	336
Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg	
100 105 110	
TGG AGA ACG GGA GTC AAA CTC ATT CCA GTT GTC TGT GAA AGC TCA AAC	384
Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn	
115 120 125	
GAT TAC CAG ATC ACC ATA GAA GCC CTG GAA GCT GCT TAT GAA ACC GCA	432
Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala	
130 135 140	
CAA GAA GCT GAC ATC AAG GTA AAG GGT TTG GTC ATA ACC AAC CCA TCA	480
Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser	
145 150 155 160	
AAC CCA CTG GGA ACA ATT ATT ACC AAG GAC ACA TTA GAA GCT CTA GTC	528
Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val	
165 170 175	

ACC TTC ACC AAC CAC AAG AAC ATT CAT CTG GTG TGT GAT GAG ATA TAT	576
Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr	
180 185 190	
GCT GGT TAC CGT CTT CAG CCC AGG GCC GAA TTC ACC AGC ATA GCC GAG	624
Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu	
195 200 205	
ATA ATT GAA GAA GAT AAA ATT TGT TGC AAT CGT GAT CTC ATC CAC ATC	672
Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile	
210 215 220	
ATT TAC AGT TTA TCC AAA GAC ATG GGA TTC CCT GGA TTT AGA GTT GGC	720
Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly	
225 230 235 240	
ATT GTG TAT TCA TAC AAT GAT GCA GTG GTG AGT TGT GCT CGT AAG ATG	768
Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met	
245 250 255	
TCG AGC TTC GGC CTA GTA TCT TCG CAA ACC CAG TAT CTG ATT GCA TCC	816
Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser	
260 265 270	
ATG TTA GCA GAC GAT GAA TTT GTA GAC AAA TTT ATT GTA GAG AGC AGA	864
Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg	
275 280 285	
AAG AGG CTG GCA ATG AGA CAT AGT TTT TTC ACA CAA AGA CTT GCT CAA	912
Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln	
290 295 300	
GTA GGC ATT AAC TGT TTA AAA AGC AAT GCT GGT CTT TTT GTG TGG ATG	960
Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met	
305 310 315 320	
GAT TTG CGT AGA CTG CTG AAA GAA CAG ACA TTT GAA GCA GAA ATG GTG	1008
Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val	
325 330 335	
TTA TGG AGA GTA ATT ATA AAC GAA ATG AAA CTC AAT GTA TCT CCT GGT	1056
Leu Trp Arg Val Ile Ile Asn Glu Met Lys Leu Asn Val Ser Pro Gly	
340 345 350	
TCG TCT TTC CAC TGC TCA GAA CCT GGC TGG TTC AGC GTC TGC TTC GCT	1104
Ser Ser Phe His Cys Ser Glu Pro Gly Trp Phe Ser Val Cys Phe Ala	
355 360 365	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu
 1 5 10 15
 Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala
 20 25 30
 Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala
 35 40 45
 Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn
 50 55 60
 Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr
 65 70 75 80
 Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg
 100 105 110
 Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn
 115 120 125
 Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala
 130 135 140
 Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val
 165 170 175
 Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu
 195 200 205
 Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile
 210 215 220
 Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly
 225 230 235 240
 Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met
 245 250 255
 Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser
 260 265 270
 Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg
 275 280 285
 Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln
 290 295 300
 Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met
 305 310 315 320

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..1098
```

CAG Gln 1	ATG Met	GGT Gly	TTT Phe	GCT Ala 5	GAA Glu	AAT Asn	CAG Gln	CTT Leu	TGC Cys 10	TTT Phe	GAT Asp	TTG Leu	ATC Ile	GAG Glu 15	AAG Lys	48
TGG Trp	GTT Val	AAA Lys	AAG Lys 20	AAT Asn	CCC Pro	AAT Asn	GCT Ala	TCC Ser 25	ATC Ile	TGC Cys	ACA Thr	GCT Ala	GAA Glu 30	GGG Gly	GTT Val	96
GAA Glu	AAC Asn	TTC Phe 35	AAG Lys	CAC His	ATA Ile	GCC Ala	AAC Asn 40	TTC Phe	CAA Gln	GAC Asp	TAT Tyr	CAT His 45	GGC Gly	CTG Leu	AAA Lys	144
GAA Glu 50	TTT Phe	AGA Arg	CAG Gln	GAA Glu	GTT Val	GCC Ala 55	AAG Lys	TTA Leu	ATG Met	GGG Gly 60	AAG Lys	GCA Ala	AGA Arg	GGC Gly	GGC Gly	192
AGA Arg 65	GTG Val	ACG Thr	TTC Phe	GAC Asp	CCA Pro 70	GAG Glu	CGT Arg	ATT Ile	GTG Val	ATG Met 75	AGC Ser	GGG Gly	GGA Gly	GCG Ala	ACA Thr 80	240
GGC Gly	GCC Ala	AGC Ser	GAG Glu	ACG Thr 85	ATT Ile	ATG Met	TTT Phe	TGC Cys	TTG Leu 90	GCG Ala	GAT Asp	CCA Pro	GGC Gly	GAT Asp 95	GCT Ala	288
CTT Leu	CTG Leu	GTT Val	CCC Pro 100	ACT Thr	CCT Pro	TAC Tyr	TAT Tyr	CCT Pro 105	GGA Gly	TTC Phe	AAT Asn	AGG Arg	GAC Asp 110	CTG Leu	AGA Arg	336
TGG Trp	CGA Arg	ACC Thr 115	GGC Gly	GTC Val	CAG Gln	ATT Ile	ATT Ile 120	CCC Pro	GTG Val	CAA Gln	TGC Cys 125	AGC Ser	AGC Ser	TCA Ser	CAC His	384

AAT	TTT	ACA	GTA	ACA	CGG	GAA	GCC	GTA	GAG	GCT	GCG	TAC	CAG	AAA	GCT	432
Asn	Phe	Thr	Val	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Gln	Lys	Ala	
	130						135				140					
CAA	GAA	GCC	AAC	ATC	AAT	GTC	ACA	GGC	TTG	ATC	ATC	ACC	AAC	CCC	TCG	480
Gln	Glu	Ala	Asn	Ile	Asn	Val	Thr	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser	
	145					150				155					160	
AAT	CCG	CTA	GGC	ACC	ACC	TTA	GAC	TCA	CAA	ACA	CTC	CAG	AGC	TTG	GTC	528
Asn	Pro	Leu	Gly	Thr	Thr	Leu	Asp	Ser	Gln	Thr	Leu	Gln	Ser	Leu	Val	
				165					170					175		
ATC	TTC	GTC	AAC	GAC	AAG	ACC	ATC	CAC	CTG	GTC	TGC	GAC	GAA	ATC	TAT	576
Ile	Phe	Val	Asn	Asp	Lys	Thr	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	
			180					185					190			
GCC	GCC	ACC	GTC	TTC	AGC	TCC	CCG	GAG	TTC	GTC	AGC	ATC	GGG	GAG	ATC	624
Ala	Ala	Thr	Val	Phe	Ser	Ser	Pro	Glu	Phe	Val	Ser	Ile	Gly	Glu	Ile	
		195					200					205				
ATC	CAA	GAA	ATG	GAC	GTC	AAC	CGC	GAC	CTT	ATC	CAC	ATC	ATC	TAC	AGC	672
Ile	Gln	Glu	Met	Asp	Val	Asn	Arg	Asp	Leu	Ile	His	Ile	Ile	Tyr	Ser	
	210					215					220					
TTG	TCC	AAA	GAT	ATG	GGT	CTC	CCC	GGT	TTC	CGG	GTA	GGT	ATT	GTG	TAT	720
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr	
	225				230				235					240		
TCC	TAC	AAC	GAC	GGT	GTA	TTA	AGC	TGC	GGC	CGG	CGG	ATG	TCG	AGC	TTT	768
Ser	Tyr	Asn	Asp	Gly	Val	Leu	Ser	Cys	Gly	Arg	Arg	Met	Ser	Ser	Phe	
				245					250					255		
GGG	TTG	GTC	TCG	TCA	CAG	ACT	CAA	TAT	TTC	CTG	GCG	ACA	CTG	CTG	TCC	816
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Ser	
			260					265					270			
GAC	GAC	GAG	TTC	GTC	GAT	TAC	TTC	CTC	CGG	GAA	AGC	TCG	AAG	AGG	CTG	864
Asp	Asp	Glu	Phe	Val	Asp	Tyr	Phe	Leu	Arg	Glu	Ser	Ser	Lys	Arg	Leu	
		275					280					285				
GCG	AGA	AGA	CAC	CAT	AAA	CTC	ACC	AGA	GGG	CTG	GAG	CAA	GTG	GGG	ATA	912
Ala	Arg	Arg	His	His	Lys	Leu	Thr	Arg	Gly	Leu	Glu	Gln	Val	Gly	Ile	
	290					295					300					
AAG	TGC	TTG	AAA	AGC	AAT	GCC	GGA	CTT	TTT	GTG	TGG	ATG	GAC	CTG	CGG	960
Lys	Cys	Leu	Lys	Ser	Asn	Ala	Gly	Leu	Phe	Val	Trp	Met	Asp	Leu	Arg	
	305				310					315				320		
AGG	CTC	CTG	GAA	GGT	CCA	ACG	TCG	TTT	GAT	GCA	GAA	ATG	AAG	CTG	TGG	1008
Arg	Leu	Leu	Glu	Gly	Pro	Thr	Ser	Phe	Asp	Ala	Glu	Met	Lys	Leu	Trp	
				325					330					335		
CGG	ACC	ATC	GTC	AAC	GAC	GTG	AAG	CTG	AAC	GTG	TCG	CCG	GGA	TCT	TCG	1056
Arg	Thr	Ile	Val	Asn	Asp	Val	Lys	Leu	Asn	Val	Ser	Pro	Gly	Ser	Ser	
			340					345					350			
TTC	CAC	GTG	GCG	GAG	CCG	GGG	TGG	TTC	AGA	GTA	TGT	TTC	GCT			1098
Phe	His	Val	Ala	Glu	Pro	Gly	Trp	Phe	Arg	Val	Cys	Phe	Ala			
		355					360					365				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln	Met	Gly	Phe	Ala	Glu	Asn	Gln	Leu	Cys	Phe	Asp	Leu	Ile	Glu	Lys	1	5	10	15
Trp	Val	Lys	Lys	Asn	Pro	Asn	Ala	Ser	Ile	Cys	Thr	Ala	Glu	Gly	Val	20	25	30	
Glu	Asn	Phe	Lys	His	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Lys	35	40	45	
Glu	Phe	Arg	Gln	Glu	Val	Ala	Lys	Leu	Met	Gly	Lys	Ala	Arg	Gly	Gly	50	55	60	
Arg	Val	Thr	Phe	Asp	Pro	Glu	Arg	Ile	Val	Met	Ser	Gly	Gly	Ala	Thr	65	70	75	80
Gly	Ala	Ser	Glu	Thr	Ile	Met	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	85	90	95	
Leu	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Gly	Phe	Asn	Arg	Asp	Leu	Arg	100	105	110	
Trp	Arg	Thr	Gly	Val	Gln	Ile	Ile	Pro	Val	Gln	Cys	Ser	Ser	Ser	His	115	120	125	
Asn	Phe	Thr	Val	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Gln	Lys	Ala	130	135	140	
Gln	Glu	Ala	Asn	Ile	Asn	Val	Thr	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser	145	150	155	160
Asn	Pro	Leu	Gly	Thr	Thr	Leu	Asp	Ser	Gln	Thr	Leu	Gln	Ser	Leu	Val	165	170	175	
Ile	Phe	Val	Asn	Asp	Lys	Thr	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	180	185	190	
Ala	Ala	Thr	Val	Phe	Ser	Ser	Pro	Glu	Phe	Val	Ser	Ile	Gly	Glu	Ile	195	200	205	
Ile	Gln	Glu	Met	Asp	Val	Asn	Arg	Asp	Leu	Ile	His	Ile	Ile	Tyr	Ser	210	215	220	
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr	225	230	235	240
Ser	Tyr	Asn	Asp	Gly	Val	Leu	Ser	Cys	Gly	Arg	Arg	Met	Ser	Ser	Phe	245	250	255	
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Ser	260	265	270	

Asp Asp Glu Phe Val Asp Tyr Phe Leu Arg Glu Ser Ser Lys Arg Leu
 275 280 285
 Ala Arg Arg His His Lys Leu Thr Arg Gly Leu Glu Gln Val Gly Ile
 290 295 300
 Lys Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg
 305 310 315 320
 Arg Leu Leu Glu Gly Pro Thr Ser Phe Asp Ala Glu Met Lys Leu Trp
 325 330 335
 Arg Thr Ile Val Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350
 Phe His Val Ala Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAG	ATG	GGC	CTT	GCC	GAG	AAT	CAG	CTT	TGC	TTT	GAT	TTG	ATC	GAA	GAC	48
Gln	Met	Gly	Leu	Ala	Glu	Asn	Gln	Leu	Cys	Phe	Asp	Leu	Ile	Glu	Asp	
1				5					10					15		
TGG	ATT	CGC	AAA	AAT	CCC	TAT	GCC	TCC	ATT	TGT	ACT	GCT	GAA	GGA	GTT	96
Trp	Ile	Arg	Lys	Asn	Pro	Tyr	Ala	Ser	Ile	Cys	Thr	Ala	Glu	Gly	Val	
			20					25					30			
GAT	GAG	TTC	AAG	GAG	ATT	GCA	AAC	TTT	CAA	GAT	TAT	CAT	GGC	TTG	CCA	144
Asp	Glu	Phe	Lys	Glu	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Pro	
			35				40					45				
GAG	TTT	AGA	AAG	GCT	GTG	GCA	AAG	TTT	ATG	GGA	AAA	GTG	AGA	GGT	GGA	192
Glu	Phe	Arg	Lys	Ala	Val	Ala	Lys	Phe	Met	Gly	Lys	Val	Arg	Gly	Gly	
	50					55					60					
AGA	GTA	ACA	TTT	GAT	CCA	GAC	CGT	ATA	GTC	ATG	GGC	GGT	GGA	GTT	ACA	240
Arg	Val	Thr	Phe	Asp	Pro	Asp	Arg	Ile	Val	Met	Gly	Gly	Gly	Val	Thr	
	65				70				75						80	
GGC	GCA	AAC	GAG	CAA	ATC	ATC	TTC	TGT	TTA	GCC	GAC	CCT	GGC	GAT	GCT	288
Gly	Ala	Asn	Glu	Gln	Ile	Ile	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	
			85						90					95		

TTT	CTT	GTT	CCC	TCA	CCT	TAT	TAT	CCA	GCA	TTT	GAC	CGG	GAC	CTG	GGA	336
Phe	Leu	Val	Pro	Ser	Pro	Tyr	Tyr	Pro	Ala	Phe	Asp	Arg	Asp	Leu	Gly	
			100					105					110			
TGG	CGC	ACT	GGA	GGT	GAA	ATA	GTT	CCT	GTT	CCC	TGT	GAC	AGC	TCA	ACC	384
Trp	Arg	Thr	Gly	Gly	Glu	Ile	Val	Pro	Val	Pro	Cys	Asp	Ser	Ser	Thr	
		115					120					125				
AAT	TTC	CAG	ATA	ACC	AGA	GAT	GCA	TTG	GAA	GAA	GCA	TAT	GAA	AAA	GCT	432
Asn	Phe	Gln	Ile	Thr	Arg	Asp	Ala	Leu	Glu	Glu	Ala	Tyr	Glu	Lys	Ala	
	130					135					140					
CGA	GAA	GCC	AAC	ATT	AAT	ATT	AAA	GGC	TTG	ATC	ATA	ACA	AAC	CCT	TCA	480
Arg	Glu	Ala	Asn	Ile	Asn	Ile	Lys	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser	
145					150					155					160	
AAC	CCA	CTT	GGC	ATC	ACC	CTA	GAC	AGA	GAT	ACT	CTT	AAA	AGC	CTA	GTG	528
Asn	Pro	Leu	Gly	Ile	Thr	Leu	Asp	Arg	Asp	Thr	Leu	Lys	Ser	Leu	Val	
			165						170					175		
AGC	TTC	ATC	GAT	GAA	AAG	AAC	ATT	CAC	TTT	GTC	TGC	GAT	GAA	ATC	TAT	576
Ser	Phe	Ile	Asp	Glu	Lys	Asn	Ile	His	Phe	Val	Cys	Asp	Glu	Ile	Tyr	
		180						185					190			
GCT	GCC	ACT	CTC	TTC	TGT	CCA	CCC	AAG	TTC	GTA	AGC	GTC	GCT	GAA	GTG	624
Ala	Ala	Thr	Leu	Phe	Cys	Pro	Pro	Lys	Phe	Val	Ser	Val	Ala	Glu	Val	
		195					200					205				
ATC	CAA	GAA	ATG	GAC	TGT	AAT	CTT	GAT	CTC	ATC	CAC	ATT	GTT	TAC	AGT	672
Ile	Gln	Glu	Met	Asp	Cys	Asn	Leu	Asp	Leu	Ile	His	Ile	Val	Tyr	Ser	
	210					215					220					
TTG	TCT	AAG	GAC	ATG	GGC	CTC	CCT	GGC	TTT	AGG	GTT	GGC	ATT	GTT	TAT	720
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr	
225					230					235					240	
TCT	TAT	AAT	GAT	GCA	GTT	GTG	AGT	TGT	ATC	CGC	AAG	ATG	TCA	AGC	TTC	768
Ser	Tyr	Asn	Asp	Ala	Val	Val	Ser	Cys	Ile	Arg	Lys	Met	Ser	Ser	Phe	
			245						250					255		
GGT	TTG	GTA	TCC	TCA	CAA	ACT	CAA	TAT	TTA	CTC	GCT	TCA	ATG	CTT	TCT	816
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Leu	Leu	Ala	Ser	Met	Leu	Ser	
			260					265					270			
GAT	GAT	GAA	TTT	GTG	GAA	AAG	TTT	CTA	GCG	GAA	AGC	TCA	AAG	AGG	CTG	864
Asp	Asp	Glu	Phe	Val	Glu	Lys	Phe	Leu	Ala	Glu	Ser	Ser	Lys	Arg	Leu	
		275					280					285				
GCA	AAA	AGG	TAC	CAT	ATT	TTC	ACA	AAG	AGA	CTT	GAG	AAA	GTG	GGG	ATT	912
Ala	Lys	Arg	Tyr	His	Ile	Phe	Thr	Lys	Arg	Leu	Glu	Lys	Val	Gly	Ile	
	290					295					300					
AAC	TGC	TTG	AAG	GGA	AAT	GCA	GGT	CTT	TTC	TTC	TGG	ATG	GAT	TTG	CGA	960
Asn	Cys	Leu	Lys	Gly	Asn	Ala	Gly	Leu	Phe	Phe	Trp	Met	Asp	Leu	Arg	
305					310					315					320	
CAC	CTC	CTT	CAA	CAA	GAA	ACA	GTT	GAT	GCC	GAA	ATG	AAG	CTA	TGG	GGC	1008
His	Leu	Leu	Gln	Gln	Glu	Thr	Val	Asp	Ala	Glu	Met	Lys	Leu	Trp	Gly	
				325					330					335		

ACG ATT TTG AAC GAT GTG AAA CTT AAC GTT TCA CCA GGC TCT TCC TTT 1056
 Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe
 340 345 350

CAT TGC CAG GAG CCT GGT TGG TTC AGA GTC TGC TTC GCT G 1096
 His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Asp
 1 5 10 15
 Trp Ile Arg Lys Asn Pro Tyr Ala Ser Ile Cys Thr Ala Glu Gly Val
 20 25 30
 Asp Glu Phe Lys Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro
 35 40 45
 Glu Phe Arg Lys Ala Val Ala Lys Phe Met Gly Lys Val Arg Gly Gly
 50 55 60
 Arg Val Thr Phe Asp Pro Asp Arg Ile Val Met Gly Gly Gly Val Thr
 65 70 75 80
 Gly Ala Asn Glu Gln Ile Ile Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Ser Pro Tyr Tyr Pro Ala Phe Asp Arg Asp Leu Gly
 100 105 110
 Trp Arg Thr Gly Gly Glu Ile Val Pro Val Pro Cys Asp Ser Ser Thr
 115 120 125
 Asn Phe Gln Ile Thr Arg Asp Ala Leu Glu Glu Ala Tyr Glu Lys Ala
 130 135 140
 Arg Glu Ala Asn Ile Asn Ile Lys Gly Leu Ile Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Ile Thr Leu Asp Arg Asp Thr Leu Lys Ser Leu Val
 165 170 175
 Ser Phe Ile Asp Glu Lys Asn Ile His Phe Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Ala Thr Leu Phe Cys Pro Pro Lys Phe Val Ser Val Ala Glu Val
 195 200 205
 Ile Gln Glu Met Asp Cys Asn Leu Asp Leu Ile His Ile Val Tyr Ser
 210 215 220

Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr
 225 230 235 240
 Ser Tyr Asn Asp Ala Val Val Ser Cys Ile Arg Lys Met Ser Ser Phe
 245 250 255
 Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Ser
 260 265 270
 Asp Asp Glu Phe Val Glu Lys Phe Leu Ala Glu Ser Ser Lys Arg Leu
 275 280 285
 Ala Lys Arg Tyr His Ile Phe Thr Lys Arg Leu Glu Lys Val Gly Ile
 290 295 300
 Asn Cys Leu Lys Gly Asn Ala Gly Leu Phe Phe Trp Met Asp Leu Arg
 305 310 315 320
 His Leu Leu Gln Gln Glu Thr Val Asp Ala Glu Met Lys Leu Trp Gly
 325 330 335
 Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe
 340 345 350
 His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAG ATG GGA TTT GGG GAA AAT CTG CTT TGC TTT GAT TTA GTT CAA GAA	48
Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu	
1 5 10 15	
TGG GTC TTA AGC AAC CCA GAA GCC TCT ATC TGC ACT GCC GAA GGT ATA	96
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile	
20 25 30	
AGT GAT TTC AGA GAT ATC GCT ATC TTT CAG GAT TAT CAC GGC TTG CCA	144
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
GAG TTC AGA AAT GCT GTT GCA AAT TTT ATG GCA AGA GTG AGA GGG AAT	192
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn	
50 55 60	

AGA	GTC	AAA	TAC	GAC	CCT	GAT	CGA	ATT	GTT	ATG	AGC	GGT	GGA	GCA	ACC	240
Arg	Val	Lys	Tyr	Asp	Pro	Asp	Arg	Ile	Val	Met	Ser	Gly	Gly	Ala	Thr	
65					70					75					80	
GGA	GCA	CAT	GAG	ACG	GTT	GCC	TTT	TGT	TTG	GCT	GAT	CCC	GGT	GAA	GCA	288
Gly	Ala	His	Glu	Thr	Val	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Glu	Ala	
			85						90						95	
TTT	TTG	GGT	GCC	ACT	CCT	TAC	TAT	CCA	GGA	TTT	GGT	CGA	GAT	TTG	AGA	336
Phe	Leu	Gly	Ala	Thr	Pro	Tyr	Tyr	Pro	Gly	Phe	Gly	Arg	Asp	Leu	Arg	
			100					105					110			
TGG	AGA	ACA	GGA	GTT	CAA	CTT	TTT	CCA	GTT	GTG	TGT	GAC	AGT	TCT	AAC	384
Trp	Arg	Thr	Gly	Val	Gln	Leu	Phe	Pro	Val	Val	Cys	Asp	Ser	Ser	Asn	
		115					120					125				
AAT	TTC	AAG	ATT	ACA	AGA	GAA	GCC	GTG	GAA	GCA	GCA	TAT	GAA	AAA	GCT	432
Asn	Phe	Lys	Ile	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Glu	Lys	Ala	
130						135					140					
CAA	GAA	GAC	CAC	ATC	AGA	ATC	AAG	GGT	TTG	GTC	CTC	ACA	AAT	CCA	TCG	480
Gln	Glu	Asp	His	Ile	Arg	Ile	Lys	Gly	Leu	Val	Leu	Thr	Asn	Pro	Ser	
145					150					155					160	
AAC	CCG	CTG	GGG	ACT	TGT	TTG	GAC	AGA	GAA	ACA	CTA	AGA	AGT	TTA	GTA	528
Asn	Pro	Leu	Gly	Thr	Cys	Leu	Asp	Arg	Glu	Thr	Leu	Arg	Ser	Leu	Val	
				165					170					175		
AGC	TTC	ATT	AAT	GAA	AAG	AAC	ATC	CAC	TTA	GTC	TGC	GAC	GAG	ATT	TAT	576
Ser	Phe	Ile	Asn	Glu	Lys	Asn	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	
		180						185					190			
GCT	GCC	ACA	ATC	TTC	ATG	GGC	CAG	CCC	GAT	TTC	ATT	AGC	ATC	TCT	GAA	624
Ala	Ala	Thr	Ile	Phe	Met	Gly	Gln	Pro	Asp	Phe	Ile	Ser	Ile	Ser	Glu	
		195					200						205			
ATT	ATA	GAA	GAA	GAT	ATT	CAC	TGC	AAT	CGC	AAT	CTC	ATC	CAC	CTT	GTT	672
Ile	Ile	Glu	Glu	Asp	Ile	His	Cys	Asn	Arg	Asn	Leu	Ile	His	Leu	Val	
210						215					220					
TAC	AGT	CTT	TCA	AAG	GAT	CTG	GGG	TTC	CCA	GGC	TTT	AGG	GTC	GGC	ATT	720
Tyr	Ser	Leu	Ser	Lys	Asp	Leu	Gly	Phe	Pro	Gly	Phe	Arg	Val	Gly	Ile	
225					230					235					240	
ATA	TAC	TCA	TAC	AAC	GAT	ACA	GTT	GTG	AGT	TGC	GCC	TGC	AAA	ATG	TCA	768
Ile	Tyr	Ser	Tyr	Asn	Asp	Thr	Val	Val	Ser	Cys	Ala	Cys	Lys	Met	Ser	
				245					250					255		
AGC	TTT	GGA	CTT	GTA	TCA	TCA	CAA	ACT	CAA	CAT	TTA	ATC	GCT	TCA	ATG	816
Ser	Phe	Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	His	Leu	Ile	Ala	Ser	Met	
			260					265					270			
TTA	TCA	GAT	GAT	GAA	TTT	GTG	GAT	AGG	TTC	ATT	ACT	GAG	AGT	GCT	AAA	864
Leu	Ser	Asp	Asp	Glu	Phe	Val	Asp	Arg	Phe	Ile	Thr	Glu	Ser	Ala	Lys	
		275					280					285				
AGG	CTT	GCA	AAA	AGG	CAC	AGA	GCC	TTC	ACA	TGG	GGG	CTA	TCT	CAA	GTA	912
Arg	Leu	Ala	Lys	Arg	His	Arg	Ala	Phe	Thr	Trp	Gly	Leu	Ser	Gln	Val	
290						295					300					

GGC ATT GGT TGT TTG AAG AGC AAT GCG GGG CTA TTT TTC TGG ATG GAT	960
Gly Ile Gly Cys Leu Lys Ser Asn Ala Gly Leu Phe Phe Trp Met Asp	
305 310 315 320	
TTG CAT CAT CTC CTC AAG GAG CAA ACT GAT GAA GCA GAG ATA GAA CTG	1008
Leu His His Leu Leu Lys Glu Gln Thr Asp Glu Ala Glu Ile Glu Leu	
325 330 335	
TGG AAA GTG ATA ATC AAC GAA GTT AAA TTA AAT GTT TCT CCG GGT TCT	1056
Trp Lys Val Ile Ile Asn Glu Val Lys Leu Asn Val Ser Pro Gly Ser	
340 345 350	
TCC TTT CAT TGC GCT AAT CCA GGA TGG TTT CGG GTT TGT TTC GCC AAC	1104
Ser Phe His Cys Ala Asn Pro Gly Trp Phe Arg Val Cys Phe Ala Asn	
355 360 365	
ATG GAC GAA	1113
Met Asp Glu	
370	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu	
1 5 10 15	
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile	
20 25 30	
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn	
50 55 60	
Arg Val Lys Tyr Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr	
65 70 75 80	
Gly Ala His Glu Thr Val Ala Phe Cys Leu Ala Asp Pro Gly Glu Ala	
85 90 95	
Phe Leu Gly Ala Thr Pro Tyr Tyr Pro Gly Phe Gly Arg Asp Leu Arg	
100 105 110	
Trp Arg Thr Gly Val Gln Leu Phe Pro Val Val Cys Asp Ser Ser Asn	
115 120 125	
Asn Phe Lys Ile Thr Arg Glu Ala Val Glu Ala Ala Tyr Glu Lys Ala	
130 135 140	
Gln Glu Asp His Ile Arg Ile Lys Gly Leu Val Leu Thr Asn Pro Ser	
145 150 155 160	

Asn Pro Leu Gly Thr Cys Leu Asp Arg Glu Thr Leu Arg Ser Leu Val
 165 170 175
 Ser Phe Ile Asn Glu Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Ala Thr Ile Phe Met Gly Gln Pro Asp Phe Ile Ser Ile Ser Glu
 195 200 205
 Ile Ile Glu Glu Asp Ile His Cys Asn Arg Asn Leu Ile His Leu Val
 210 215 220
 Tyr Ser Leu Ser Lys Asp Leu Gly Phe Pro Gly Phe Arg Val Gly Ile
 225 230 235 240
 Ile Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Cys Lys Met Ser
 245 250 255
 Ser Phe Gly Leu Val Ser Ser Gln Thr Gln His Leu Ile Ala Ser Met
 260 265 270
 Leu Ser Asp Asp Glu Phe Val Asp Arg Phe Ile Thr Glu Ser Ala Lys
 275 280 285
 Arg Leu Ala Lys Arg His Arg Ala Phe Thr Trp Gly Leu Ser Gln Val
 290 295 300
 Gly Ile Gly Cys Leu Lys Ser Asn Ala Gly Leu Phe Phe Trp Met Asp
 305 310 315 320
 Leu His His Leu Leu Lys Glu Gln Thr Asp Glu Ala Glu Ile Glu Leu
 325 330 335
 Trp Lys Val Ile Ile Asn Glu Val Lys Leu Asn Val Ser Pro Gly Ser
 340 345 350
 Ser Phe His Cys Ala Asn Pro Gly Trp Phe Arg Val Cys Phe Ala Asn
 355 360 365
 Met Asp Glu
 370

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAYTTYGAYG GNTGGAARGC

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCRTCCATRT TNGCRAARCA

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CARATGGGNY TNGCNGARAA

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCRAARCANA CNCKRAACCA

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTGATCARA TGGGNYTNGC NGARAA

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCTGCAGCR AARCANACNC KRAACCA

27